

TL- $\gamma$  amino acid sequence (SEQ ID NO:1)

5	M	S	G	G	G	N	I	K	V	V	V	R	V	R	P	F	N	A	R	E	I
	D	R	G	A	K	C	I	V	R	M	E	G	N	Q	T	I	L	T	P	P	P
	G	A	E	E	K	A	R	K	S	G	K	T	I	M	D	G	P	K	A	F	A
	F	D	R	S	Y	W	S	F	D	K	N	A	P	N	Y	A	R	Q	E	D	L
	F	Q	D	L	G	V	P	L	L	D	N	A	F	K	G	Y	N	N	C	I	F
10	A	Y	G	Q	T	G	S	G	K	S	Y	S	M	M	G	Y	G	K	E	H	G
	V	I	P	R	I	C	Q	D	M	F	R	R	I	N	E	L	Q	K	D	K	N
	L	T	C	T	V	E	V	S	Y	L	E	I	Y	N	E	R	V	R	D	L	L
	N	P	S	T	K	G	N	L	K	V	R	E	H	P	S	T	G	P	Y	V	E
	D	L	A	K	L	V	V	R	S	F	Q	E	I	E	N	L	M	D	E	G	N
15	K	A	R	T	V	A	A	T	N	M	N	E	T	S	S	R	S	H	A	V	F
	T	L	T	L	T	Q	K	W	H	D	E	E	T	K	M	D	T	E	K	V	A
	K	I	S	L	V	D	L	A	G	S	E	R	A	T	S	T	G	A	T	G	A
	R	L	K	E	G	A	E	I	N	R	S	L	S	T	L	G	R	V	I	A	A
	L	A	D	M	S	S	G	K	Q	K	K	N	Q	L	V	P	Y	R	D	S	V
20	L	T	W	L	L	K	D	S	L	G	G	N	S	M	T	A	M	I	A	A	I
	S	P	A	D	I	N	F	E	E	T	L	S	T	L	R	Y	A	D	S	A	K
	R	I	K	N	H	A	V	V	N	E	D	P	N	A	R	M	I	R	E	L	K
	E	E	L	A	Q	L	R	S	K	L	Q	S	S	G	G	G	G	G	A	G	
	G	S	G	G	P	V	E	E	S	Y	P	P	D	T	P	L	E	K	Q	I	V
25	S	I	Q	Q	P	D	A	T	V	K	K	M	S	K	A	E	I	V	E	Q	L
	N	Q	S	E	K	L	Y	R	D	L	N	Q	T	W	E	E	K	L	A	K	T
	E	E	I	H	K	E	R	E	A	A	L	E	E	L	G	I	S	I	E	K	G
	F	V	G	P	Y	H	S	K	E	M	P	H	L	V	N	L	S	D	D	P	L
	L	A	E	C	L	V	Y	N	I	K	P	G	Q	T	R	V	G	N	V	N	Q
30	D	T	Q	A	E	I	R	L	N	G	S	K	I	L	K	E	H	C	T	F	E
	N	V	D	N	V	V	T	I	V	P	N	E	K	A	A	V	M	V	N	G	V
	R	I	D	K	P	T	R	L	R	S	G	Y	R	I	I	L	G	D	F	H	I
	F	R	F	N	H	P	E	E	A	R	A	E	R	Q	E	Q	S	L	L	R	H
	S	V	T	N	S	Q	L	G	S	P	A	P	G	R	H	D	R	T	L	S	K
35	A	G	S	D	A	D	G	D	S	R	S	D	S	P	L	P	H	F	R	G	K
	D	S	D	W	F	Y	A	R	R	E	A	A	S	A	I	L	G	L	D	Q	K
	I	S	H	L	T	D	D	E	L	D	A	L	F	D	D	V	Q	K	A	R	A

V R R G L V E D N E D S D S Q S S F P V R  
 D K Y M S N G T I D N F S L D T A I T M P  
 G T P R S D D D G D A L F F G D K K S K Q  
 D A S N V D V E E L R Q Q Q A Q M E E A L  
 5 K T A K Q E F

TL- $\gamma$  nucleotide sequence (SEQ ID NO:2)

ATGTCGGGCGGTGGAAATATCAAGGTGGTGGTGCGGGTACGCCC GTTCAA  
 10 CGCCCCGAGAAATCGACCGTGGCGCAAAATGTATTGTGCGGATGGAAGGAA  
 ATCAAACCATCCTCACCCCTCCTCCGGGTGCCGAAGAGAAGGCGCGTAAA  
 AGTGGCAAAACTATTATGGATGGCCCGAAGGCATTTGCGTTCGATCGGTC  
 GTATTGGTCCTTTGACAAGAATGCTCCCAACTATGCGAGACAGGAAGACC  
 TATTCCAAGATCTCGGAGTCCCGCTTCTGGATAATGCATTCAAGGGTTAT  
 15 AACAATTGTATCTTCGCCTACGGTCAGACCGGTTCCGGGCAAGTCCTATTC  
 AATGATGGGCTATGGCAAGGAGCATGGCGTGATCCCGCGGATTTGCCAGG  
 ACATGTTCCGGCGTATTAATGAACTGCAGAAGGACAAGAACCTCACTTGC  
 ACCGTCGAAGTTTCGTACTTGGAAATTTACAATGAACGAGTGCGAGACTT  
 GCTGAATCCGTCGACAAAGGGGAATCTCAAGGTCCGAGAACACCCGTCGA  
 20 CCGGCCCCCTACGTGGAGGACTTGGCGAAGCTGGTTCGTGCGATCATTCCAA  
 GAAATCGAAAATCTCATGGATGAGGGCAACAAAGCCAGAACGGTTGCCGC  
 CACAAACATGAACGAGACATCCAGTCGATCCACGCCGTCTTCACTTTGA  
 CCTTGACGCAAAAGTGGCATGATGAAGAGACCAAAATGGACACAGAGAAG  
 GTTGCGAAGATCAGTCTGGTAGATTTGGCGGGTTCTGAGCGAGCAACGTC  
 25 CACCGGAGCTACTGGAGCGCGACTGAAGGAGGGTGCAGAGATCAACCGCT  
 CACTTTCGACCCTAGGTCGTGTGATTGCAGCGCTAGCGGATATGTCGTGC  
 GGAAAACAGAAGAAGAATCAGTTAGTACCTTACCGAGATTCGGTACTGAC  
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 CCGCCATTTTCGCTGCTGATATTAACCTTGAAGAGACTCTCAGTACCCTT  
 30 CGATATGCGGACTCTGCGAAGCGAATCAAGAACCACGCAGTGGTCAATGA  
 AGACCCGAACGCGCGGATGATCCGCGAGTTGAAGGAGGAACTCGCGCAGC  
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 GCAAATCGTGTGATTTCAGCAGCCGGATGCGACAGTCAAGAAAATGAGCA  
 35 AGGCAGAAATCGTGGAGCAACTGAACCAGAGTGAGAAGCTCTATCGGGAT  
 CTCAATCAGACCTGGGAAGAGAAGCTGGCCAAGACCGAGGAAATCCACAA  
 GGAACGAGAAGCGGCGCTCGAGGAGCTGGGTATCAGCATCGAAAAGGGCT

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